SEQUENCE LISTING

<110> St.George-Hyslop, Peter H.
Fraser, Paul E.
Schering-Plough Corporation

<120> A novel presenilin associated membrane protein and uses thereof

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Ser Met Phe Asn Lys Pro Lys Glu Asp Gly Ser Ser Gly Tyr Pro Tyr
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Cys Gly Met Ser Phe Arg Leu Ala Asn Met Ala Ala Gly Asn Ser Glu
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Gly Asn Ser Val Glu Arg Lys Ile Tyr Ile Pro Leu Asn Lys Thr Ala
        35                  40                  45
Pro Cys Val Arg Leu Leu Asn Ala Thr His Gln Ile Gly Cys Gln Ser
    50                  55                  60
Ser Ile Ser Gly Asp Thr Gly Val Ile His Val Val Glu Lys Glu Glu
65                  70                  75                  80
Asp Leu Gln Trp Val Leu Thr Asp Gly Pro Asn Pro Pro Tyr Met Val
                85                  90                  95
Leu Leu Glu Ser Lys His Phe Thr Arg Asp Leu Met Glu Lys Leu Lys
            100                 105                 110
Gly Arg Thr Ser Arg Ile Ala Gly Leu Ala Val Ser Leu Thr Lys Pro
        115                 120                 125
Ser Pro Ala Ser Gly Phe Ser Pro Ser Val Gln Cys Pro Asn Asp Gly
    130                 135                 140
Phe Gly Val Tyr Ser Asn Ser Tyr Gly Pro Glu Phe Ala His Cys Arg
```

```
145                 150                 155                 160
Glu Ile Gln Trp Asn Ser Leu Gly Asn Gly Leu Ala Tyr Glu Asp Phe
                165                 170                 175
Ser Phe Pro Ile Phe Leu Leu Glu Asp Glu Asn Glu Thr Lys Val Ile
            180                 185                 190
Lys Gln Cys Tyr Gln Asp His Asn Leu Ser Gln Asn Gly Ser Ala Pro
        195                 200                 205
Thr Phe Pro Leu Cys Ala Met Gln Leu Phe Ser His Met His Ala Val
    210                 215                 220
Ile Ser Thr Ala Thr Cys Met Arg Arg Ser Ser Ile Gln Ser Thr Phe
225                 230                 235                 240
Ser Ile Asn Pro Glu Ile Val Cys Asp Pro Leu Ser Asp Tyr Asn Val
                245                 250                 255
Trp Ser Met Leu Lys Pro Ile Asn Thr Thr Gly Thr Leu Lys Pro Asp
            260                 265                 270
Asp Arg Val Val Val Ala Ala Thr Arg Leu Asp Ser Arg Ser Phe Phe
        275                 280                 285
Trp Asn Val Ala Pro Gly Ala Glu Ser Ala Val Ala Ser Phe Val Thr
    290                 295                 300
Gln Leu Ala Ala Ala Glu Ala Leu Gln Lys Ala Pro Asp Val Thr Thr
305                 310                 315                 320
Leu Pro Arg Asn Val Met Phe Val Phe Phe Gln Gly Glu Thr Phe Asp
                325                 330                 335
Tyr Ile Gly Ser Ser Arg Met Val Tyr Asp Met Glu Lys Gly Lys Phe
            340                 345                 350
Pro Val Gln Leu Glu Asn Val Asp Ser Phe Val Glu Leu Gly Gln Val
        355                 360                 365
Ala Leu Arg Thr Ser Leu Glu Leu Trp Met His Thr Asp Pro Val Ser
    370                 375                 380
Gln Lys Asn Glu Ser Val Arg Asn Gln Val Glu Asp Leu Leu Ala Thr
385                 390                 395                 400
Leu Glu Lys Ser Gly Ala Gly Val Pro Ala Val Ile Leu Arg Arg Pro
                405                 410                 415
Asn Gln Ser Gln Pro Leu Pro Pro Ser Ser Leu Gln Arg Phe Leu Arg
            420                 425                 430
Ala Arg Asn Ile Ser Gly Val Val Leu Ala Asp His Ser Gly Ala Phe
        435                 440                 445
His Asn Lys Tyr Tyr Gln Ser Ile Tyr Asp Thr Ala Glu Asn Ile Asn
    450                 455                 460
Val Ser Tyr Pro Glu Trp Leu Ser Pro Glu Glu Asp Leu Asn Phe Val
465                 470                 475                 480
Thr Asp Thr Ala Lys Ala Leu Ala Asp Val Ala Thr Val Leu Gly Arg
                485                 490                 495
Ala Leu Tyr Glu Leu Ala Gly Gly Thr Asn Phe Ser Asp Thr Val Gln
            500                 505                 510
Ala Asp Pro Gln Thr Val Thr Arg Leu Leu Tyr Gly Phe Leu Ile Lys
        515                 520                 525
Ala Asn Asn Ser Trp Phe Gln Ser Ile Leu Arg Gln Asp Leu Arg Ser
    530                 535                 540
Tyr Leu Gly Asp Gly Pro Leu Gln His Tyr Ile Ala Val Ser Ser Pro
545                 550                 555                 560
Thr Asn Thr Thr Tyr Val Val Gln Tyr Ala Leu Ala Asn Leu Thr Gly
                565                 570                 575
Thr Val Val Asn Leu Thr Arg Glu Gln Cys Gln Asp Pro Ser Lys Val
            580                 585                 590
Pro Ser Glu Asn Lys Asp Leu Tyr Glu Tyr Ser Trp Val Gln Gly Pro
        595                 600                 605
Leu His Ser Asn Glu Thr Asp Arg Leu Pro Arg Cys Val Arg Ser Thr
    610                 615                 620
Ala Arg Leu Ala Arg Ala Leu Ser Pro Ala Phe Glu Leu Ser Gln Trp
```

```
625                 630                 635                 640
Ser Ser Thr Glu Tyr Ser Thr Trp Thr Glu Ser Arg Trp Lys Asp Ile
                645                 650                 655
Arg Ala Arg Ile Phe Leu Ile Ala Ser Lys Glu Leu Glu Leu Ile Thr
            660                 665                 670
Leu Thr Val Gly Phe Gly Ile Leu Ile Phe Ser Leu Ile Val Thr Tyr
        675                 680                 685
Cys Ile Asn Ala Lys Ala Asp Val Leu Phe Ile Ala Pro Arg Glu Pro
    690                 695                 700
Gly Ala Val Ser Tyr
705
```

<210> 15
<211> 2250
<212> DNA
<213> mouse

<400> 15

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cccagcggag aggcaacatg gctacgacta ggggcggctc tgggcctgac ccaggaagtc      60
ggggtcttct tcttctgtct ttttccgtgg tactggcagg attgtgtggg ggaaactcag     120
tggagaggaa aatctacatt ccccttaaata aaacagctcc ttgtgtccgc ctgctcaacg     180
ccactcatca gattggctgc cagtcttcaa ttagtgggga tacaggggtt atccacgtag     240
tggagaaaga agaagacctg aagtgggtgt tgaccgatgg ccccaacccc ccttacatgg     300
ttctgctgga gggcaagctc ttcaccagag atgtaatgga gaagctgaag ggaacaacca     360
gtagaatcgc tggtcttgcc gtgactctag ccaagcccaa ctcaacttca agcttctctc     420
ctagtgtgca gtgcccaaat gatgggtttg gtatttactc caactcctac gggccagagt     480
ttgctcactg caagaaaaca ctgtggaatg aactgggcaa cggcttggct tatgaagact     540
ttagtttccc catctttctt cttgaagatg agaacgaaac caaggtcatc aagcagtgct     600
atcaagatca caacctgggt cagaatggct ctgcaccaag cttcccattg tgtgctatgc     660
agctcttctc acacatgcac gccgtcatca gcactgccac ctgcatgcgg cgcagcttca     720
tccagagcac cttcagcatc aacccagaaa tcgtctgtga ccccttatct gactacaacg     780
tatggagcat gcttaagcct ataaatacat ctgtgggact agaacctgac gtcagggttg     840
tggttgcggc cacacggctg gatagccggt ccttttttctg gaatgtggcc ccaggggctg     900
aaagtgctgt agcctccttt gtcactcagc tggctgcagc tgaagctttg cacaaggcac     960
ctgatgtgac cactctatcc cgaaatgtga tgtttgtctt cttccagggg gaaacttttg    1020
actacattgg cagctcacgg atggtctatg atatggagaa cggcaagttt cccgtgcggc    1080
tcgagaacat cgactccttc gtggagctgg gacaggtggc cctaagaact tcactagatc    1140
tctggatgca cacagatccc atgtctcaga aaaatgagtc tgtgaaaaac caggtggagg    1200
atcttctggc cactctggag aagagcggtg ctggtgtccc tgaagttgtc ctgaggagac    1260
tggcccagtc ccaggccctt ccaccttcat ctctacaacg atttcttcgg gctcgaaaca    1320
tctctggcgt ggtcctggct gaccactctg gctccttcca caatcggtat taccagagca    1380
tttatgacac ggctgagaac attaatgtga cctatcctga gtggcagagc ccagaagagg    1440
acctcaactt tgtgacagac actgccaagg cactggcgaa tgtggccaca gtgctggcgc    1500
gtgcactgta tgagcttgca ggaggaacca acttcagcag ctccatccag gctgatcccc    1560
agacagttac acgtctgctc tatgggttcc tggttaaagc taacaactca tggtttcagt    1620
cgatcctgaa acatgaccta aggtcctatt tggatgacag gcctcttcaa cactacatcg    1680
ccgtctccag ccctaccaac acgacttacg ttgtgcagta cgccttggca aacctgactg    1740
gcaaggcgac caacctcacc cgagagcagt gccaggatcc aagtaaagtc ccaaatgaga    1800
gcaaggattt atatgaatac tcgtgggtac aaggcccttg gaattccaac aggacagaga    1860
ggctcccaca gtgtgtgcgc tccacagtgc gactggccag ggccttgtcc cctgcctttg    1920
aactgagtca gtggagctcc acagaatact ctacgtgggc ggagagccgc tggaaagaca    1980
tccaagctcg gatattccta attgccagca aaaagcttga gttcatcacg ctgatcgtgg    2040
gcttcagcat ccttatcttc tctctcatcg tcacctactg catcaatgcc aaagccgacg    2100
tcctttygt tgctccccga gagccaggag ctgtgtctta ctgaagagga ctctagctct    2160
ccctgcctgc tctgaacttt acttcccaga ccaggtgtcc ggctgggaac aaaccactaa    2220
tttgtcactg gactgtctct gggcctgctt                                    2250
```

<210> 16
<211> 708
<212> PRT

<213> mouse

<400> 16

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Met Ala Thr Thr Arg Gly Gly Ser Gly Pro Asp Pro Gly Ser Arg Gly
 1               5                  10                  15
Leu Leu Leu Leu Ser Phe Ser Val Val Leu Ala Gly Leu Cys Gly Gly
            20                  25                  30
Asn Ser Val Glu Arg Lys Ile Tyr Ile Pro Leu Asn Lys Thr Ala Pro
        35                  40                  45
Cys Val Arg Leu Leu Asn Ala Thr His Gln Ile Gly Cys Gln Ser Ser
    50                  55                  60
Ile Ser Gly Asp Thr Gly Val Ile His Val Val Glu Lys Glu Glu Asp
65                  70                  75                  80
Leu Lys Trp Val Leu Thr Asp Gly Pro Asn Pro Pro Tyr Met Val Leu
                85                  90                  95
Leu Glu Gly Lys Leu Phe Thr Arg Asp Val Met Glu Lys Leu Lys Gly
            100                 105                 110
Thr Thr Ser Arg Ile Ala Gly Leu Ala Val Thr Leu Ala Lys Pro Asn
        115                 120                 125
Ser Thr Ser Ser Phe Ser Pro Ser Val Gln Cys Pro Asn Asp Gly Phe
    130                 135                 140
Gly Ile Tyr Ser Asn Ser Tyr Gly Pro Glu Phe Ala His Cys Lys Lys
145                 150                 155                 160
Thr Leu Trp Asn Glu Leu Gly Asn Gly Leu Ala Tyr Glu Asp Phe Ser
                165                 170                 175
Phe Pro Ile Phe Leu Leu Glu Asp Glu Asn Glu Thr Lys Val Ile Lys
            180                 185                 190
Gln Cys Tyr Gln Asp His Asn Leu Gly Gln Asn Gly Ser Ala Pro Ser
        195                 200                 205
Phe Pro Leu Cys Ala Met Gln Leu Phe Ser His Met His Ala Val Ile
    210                 215                 220
Ser Thr Ala Thr Cys Met Arg Arg Ser Phe Ile Gln Ser Thr Phe Ser
225                 230                 235                 240
Ile Asn Pro Glu Ile Val Cys Asp Pro Leu Ser Asp Tyr Asn Val Trp
                245                 250                 255
Ser Met Leu Lys Pro Ile Asn Thr Ser Val Gly Leu Glu Pro Asp Val
            260                 265                 270
Arg Val Val Val Ala Ala Thr Arg Leu Asp Ser Arg Ser Phe Phe Trp
        275                 280                 285
Asn Val Ala Pro Gly Ala Glu Ser Ala Val Ala Ser Phe Val Thr Gln
    290                 295                 300
Leu Ala Ala Ala Glu Ala Leu His Lys Ala Pro Asp Val Thr Thr Leu
305                 310                 315                 320
Ser Arg Asn Val Met Phe Val Phe Phe Gln Gly Glu Thr Phe Asp Tyr
                325                 330                 335
Ile Gly Ser Ser Arg Met Val Tyr Asp Met Glu Asn Gly Lys Phe Pro
            340                 345                 350
Val Arg Leu Glu Asn Ile Asp Ser Phe Val Glu Leu Gly Gln Val Ala
        355                 360                 365
Leu Arg Thr Ser Leu Asp Leu Trp Met His Thr Asp Pro Met Ser Gln
    370                 375                 380
Lys Asn Glu Ser Val Lys Asn Gln Val Glu Asp Leu Leu Ala Thr Leu
385                 390                 395                 400
Glu Lys Ser Gly Ala Gly Val Pro Glu Val Val Leu Arg Arg Leu Ala
                405                 410                 415
Gln Ser Gln Ala Leu Pro Pro Ser Ser Leu Gln Arg Phe Leu Arg Ala
            420                 425                 430
Arg Asn Ile Ser Gly Val Val Leu Ala Asp His Ser Gly Ser Phe His
        435                 440                 445
Asn Arg Tyr Tyr Gln Ser Ile Tyr Asp Thr Ala Glu Asn Ile Asn Val
```

```
    450                 455                 460
Thr Tyr Pro Glu Trp Gln Ser Pro Glu Glu Asp Leu Asn Phe Val Thr
465                 470                 475                 480
Asp Thr Ala Lys Ala Leu Ala Asn Val Ala Thr Val Leu Ala Arg Ala
                485                 490                 495
Leu Tyr Glu Leu Ala Gly Gly Thr Asn Phe Ser Ser Ser Ile Gln Ala
            500                 505                 510
Asp Pro Gln Thr Val Thr Arg Leu Leu Tyr Gly Phe Leu Val Lys Ala
        515                 520                 525
Asn Asn Ser Trp Phe Gln Ser Ile Leu Lys His Asp Leu Arg Ser Tyr
    530                 535                 540
Leu Asp Asp Arg Pro Leu Gln His Tyr Ile Ala Val Ser Ser Pro Thr
545                 550                 555                 560
Asn Thr Thr Tyr Val Val Gln Tyr Ala Leu Ala Asn Leu Thr Gly Lys
                565                 570                 575
Ala Thr Asn Leu Thr Arg Glu Gln Cys Gln Asp Pro Ser Lys Val Pro
            580                 585                 590
Asn Glu Ser Lys Asp Leu Tyr Glu Tyr Ser Trp Val Gln Gly Pro Trp
        595                 600                 605
Asn Ser Asn Arg Thr Glu Arg Leu Pro Gln Cys Val Arg Ser Thr Val
    610                 615                 620
Arg Leu Ala Arg Ala Leu Ser Pro Ala Phe Glu Leu Ser Gln Trp Ser
625                 630                 635                 640
Ser Thr Glu Tyr Ser Thr Trp Ala Glu Ser Arg Trp Lys Asp Ile Gln
                645                 650                 655
Ala Arg Ile Phe Leu Ile Ala Ser Lys Lys Leu Glu Phe Ile Thr Leu
            660                 665                 670
Ile Val Gly Phe Ser Ile Leu Ile Phe Ser Leu Ile Val Thr Tyr Cys
        675                 680                 685
Ile Asn Ala Lys Ala Asp Val Leu Phe Val Ala Pro Arg Glu Pro Gly
    690                 695                 700
Ala Val Ser Tyr
705
```

<210> 17
<211> 2942
<212> DNA
<213> D. melanogaster

<400> 17

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tctgatatca tcgccactgt gctgggaatt cggcacgagc gcaacactgc aatttctgga      60
cgcgatttcg tgggaatctt cgatggaaat gcgtctgaat gcggcttcca tatggctgtt     120
aatactgtcg tatggagcaa ctattgctca aggagaaaga acccgcgata agatgtacga     180
gcccattgga ggagctagct gtttccgacg gctgaatggc acccatcaga caggctgttc     240
ctcaacctac tccggttccg tgggcgtact acatctaata aacgtcgagg ccgacctgga     300
atttcttctt agcagcccac catctccacc ttacgccccc atgataccac ctcacctgtt     360
cacacgtaac aacctgatgc gcctaaagga agccggacca aagaacattt ctgtggtgct     420
gctgatcaac cgcacgaacc agatgaagca gttctcgcac gaactcaact gccccaatca     480
gtacagcggc ctgaacagca ccagtgagac ctgcgacgcc agcaatccag ccaaaaactg     540
gaatccctgg ggcactggac ttctgcacga ggactttccc tttcctatct attacatagc     600
cgatttggat caggtcacca agctagagaa gtgctttcag gactttaaca accataacta     660
cgagacgcac gcgctgcgta gcttgtgcgc cgtcgaggtc aagtccttta tgtccgccgc     720
tgtcaacacc gaggtctgta tgcgccgcac caacttcatc aataatcttg gaggaagcaa     780
gtactgcgat ccgctcgagg gacggaatgt ttcgccacct tgtacccccg aaagccagca     840
atcggaaaca actttggaga cagtccatac gaatgaaaag ttcatattag taacctgtcg     900
cctggacacc accaccatgt tcgatggcgt cggtcttgga gccatggact ccctcatggg     960
atttgctgtt ttcactcatg tggcgtatct attaaaacaa ctacttccgc cgcaaagcaa    1020
agaccttcat aatgtcctct ttgtgacttt taatggcgaa tcctatgact acattggttc    1080
tcaaagattt gtatacgaca tggagaaact tcaatttcct actgaatcca caggcacgcc    1140
tccgattgcc tttgacaata ttgacttcat gctggacatc gggacactgg atgacatatc    1200
```

```
gaatattaag ctgcatgcgt taaatggaac gactttggct cagcaaattc tagagcggct    1260
aaataactat gcgaagtcgc cacgctatgg ctttaacctg aacattcagt ccgagatgag    1320
cgctcactta ccacctacgt cggcgcaatc atttctgcga cgtgatccaa acttcaatgc    1380
attgattcta aacgctcgtc caacgaacaa gtattatcat tccacatacg atgacgcgga    1440
taacgtggac ttcacctatg cgaacacaag caaggatttc acccagctga cggaagttaa    1500
tgactttaaa agcttgaacc cagattcact gcaaatgaaa gtgcgcaacg tttcctctat    1560
tgtggccatg gccctatatc agacaataac tggaaaggag tacactggca ccaaggtggc    1620
caaccctctg atggcagatg agttccttta ctgtttcctg caatcggcgg actgcccact    1680
ctttaaggcc gcatcttatc cgggcagtca gctcaccaat ttgcctccga tgcgctacat    1740
aagcgtcttg ggtggctctc aagagtcgtc gggctatacg tatagattgc tgggctatct    1800
cttgtcacaa ctgcagccag acattcacag agataactgc accgacttgc cgctgcacta    1860
tttcgccgga ttcaacaata tcggagagtg tcgcctcacc acgcagaact acagtcacgc    1920
cctgagtcca gcttttctta ttgatggcta cgattggagt tccggcatgt attccacttg    1980
gactgaatcc acctggtcac agttcagtgc acgcatcttc ctgcgcccgt ccaatgtgca    2040
ccaggtcaca actctaagcg ttggcatagt ggtgctgata atatccttct gtttggtgta    2100
tataatcagc tcacgatcgg aagtcctctt tgaggatttg ccggcaagca atgccgcatt    2160
atttggttga tgtcacaact gccacagcga cgaaatcatc gcgttcagca gctcattcca    2220
tagatttctg catgcgtaaa ctaaacgtta cttgtaaacc aatcgattaa gaatttctga    2280
ttgtgccctt ttagatcgcc gcggccgaca gcctgttaaa tcttcaaaga atatctgatc    2340
acgtgccgaa gatgattggt tgctgaatat gatctaaaac aaaaaacaga cttaacaaag    2400
acactaaaat gatattctaa ctcgtcttat ttaaaacatt aagcaaacgt ttatttatat    2460
gtatttttgt attttaaagt agtaaattag cttctatcaa ctacgttgta tcatatatag    2520
acatttaacc aattgcgaca aaattctttc cacttgtccg gccctttttg cattgtacat    2580
aggattaacc aacccaattg aacctctgat aatgccaagg aagagatgtc tgtacaaata    2640
ttgacaagaa actgctataa cttataaatc actggaaata tttatacctt ctgcatctat    2700
tgcgatactg aacttaatga tctgaaatca ttacttcata gaagacaaat aattattata    2760
acgactttaa attatatatg tttaataaat tttgataagg tgtaaagcaa tgtcctgtta    2820
tctagttagg ttattttcaa ggcaattatt cacagctctc agattccaac gattgatgta    2880
gtttaatctc aactctttac caaagaagtc catttgtact agtgtaaaag atattttcaa    2940
ta                                                                   2942
```

<210> 18
<211> 695
<212> PRT
<213> D. melanogaster

<400> 18

```
Met Glu Met Arg Leu Asn Ala Ala Ser Ile Trp Leu Leu Ile Leu Ser
 1               5                  10                  15
Tyr Gly Ala Thr Ile Ala Gln Gly Glu Arg Thr Arg Asp Lys Met Tyr
            20                  25                  30
Glu Pro Ile Gly Gly Ala Ser Cys Phe Arg Arg Leu Asn Gly Thr His
        35                  40                  45
Gln Thr Gly Cys Ser Ser Thr Tyr Ser Gly Ser Val Gly Val Leu His
    50                  55                  60
Leu Ile Asn Val Glu Ala Asp Leu Glu Phe Leu Leu Ser Ser Pro Pro
65                  70                  75                  80
Ser Pro Pro Tyr Ala Pro Met Ile Pro Pro His Leu Phe Thr Arg Asn
                85                  90                  95
Asn Leu Met Arg Leu Lys Glu Ala Gly Pro Lys Asn Ile Ser Val Val
            100                 105                 110
Leu Leu Ile Asn Arg Thr Asn Gln Met Lys Gln Phe Ser His Glu Leu
        115                 120                 125
Asn Cys Pro Asn Gln Tyr Ser Gly Leu Asn Ser Thr Ser Glu Thr Cys
    130                 135                 140
Asp Ala Ser Asn Pro Ala Lys Asn Trp Asn Pro Trp Gly Thr Gly Leu
145                 150                 155                 160
Leu His Glu Asp Phe Pro Phe Pro Ile Tyr Tyr Ile Ala Asp Leu Asp
                165                 170                 175
Gln Val Thr Lys Leu Glu Lys Cys Phe Gln Asp Phe Asn Asn His Asn
```

```
            180                 185                 190
Tyr Glu Thr His Ala Leu Arg Ser Leu Cys Ala Val Glu Val Lys Ser
        195                 200                 205
Phe Met Ser Ala Ala Val Asn Thr Glu Val Cys Met Arg Arg Thr Asn
    210                 215                 220
Phe Ile Asn Asn Leu Gly Gly Ser Lys Tyr Cys Asp Pro Leu Glu Gly
225                 230                 235                 240
Arg Asn Val Ser Pro Pro Cys Thr Pro Glu Ser Gln Gln Ser Glu Thr
                245                 250                 255
Thr Leu Glu Thr Val His Thr Asn Glu Lys Phe Ile Leu Val Thr Cys
            260                 265                 270
Arg Leu Asp Thr Thr Thr Met Phe Asp Gly Val Gly Leu Gly Ala Met
        275                 280                 285
Asp Ser Leu Met Gly Phe Ala Val Phe Thr His Val Ala Tyr Leu Leu
    290                 295                 300
Lys Gln Leu Leu Pro Pro Gln Ser Lys Asp Leu His Asn Val Leu Phe
305                 310                 315                 320
Val Thr Phe Asn Gly Glu Ser Tyr Asp Tyr Ile Gly Ser Gln Arg Phe
                325                 330                 335
Val Tyr Asp Met Glu Lys Leu Gln Phe Pro Thr Glu Ser Thr Gly Thr
            340                 345                 350
Pro Pro Ile Ala Phe Asp Asn Ile Asp Phe Met Leu Asp Ile Gly Thr
        355                 360                 365
Leu Asp Asp Ile Ser Asn Ile Lys Leu His Ala Leu Asn Gly Thr Thr
    370                 375                 380
Leu Ala Gln Gln Ile Leu Glu Arg Leu Asn Asn Tyr Ala Lys Ser Pro
385                 390                 395                 400
Arg Tyr Gly Phe Asn Leu Asn Ile Gln Ser Glu Met Ser Ala His Leu
                405                 410                 415
Pro Pro Thr Ser Ala Gln Ser Phe Leu Arg Arg Asp Pro Asn Phe Asn
            420                 425                 430
Ala Leu Ile Leu Asn Ala Arg Pro Thr Asn Lys Tyr Tyr His Ser Thr
        435                 440                 445
Tyr Asp Asp Ala Asp Asn Val Asp Phe Thr Tyr Ala Asn Thr Ser Lys
    450                 455                 460
Asp Phe Thr Gln Leu Thr Glu Val Asn Asp Phe Lys Ser Leu Asn Pro
465                 470                 475                 480
Asp Ser Leu Gln Met Lys Val Arg Asn Val Ser Ser Ile Val Ala Met
                485                 490                 495
Ala Leu Tyr Gln Thr Ile Thr Gly Lys Glu Tyr Thr Gly Thr Lys Val
            500                 505                 510
Ala Asn Pro Leu Met Ala Asp Glu Phe Leu Tyr Cys Phe Leu Gln Ser
        515                 520                 525
Ala Asp Cys Pro Leu Phe Lys Ala Ala Ser Tyr Pro Gly Ser Gln Leu
    530                 535                 540
Thr Asn Leu Pro Pro Met Arg Tyr Ile Ser Val Leu Gly Gly Ser Gln
545                 550                 555                 560
Glu Ser Ser Gly Tyr Thr Tyr Arg Leu Leu Gly Tyr Leu Leu Ser Gln
                565                 570                 575
Leu Gln Pro Asp Ile His Arg Asp Asn Cys Thr Asp Leu Pro Leu His
            580                 585                 590
Tyr Phe Ala Gly Phe Asn Asn Ile Gly Glu Cys Arg Leu Thr Thr Gln
        595                 600                 605
Asn Tyr Ser His Ala Leu Ser Pro Ala Phe Leu Ile Asp Gly Tyr Asp
    610                 615                 620
Trp Ser Ser Gly Met Tyr Ser Thr Trp Thr Glu Ser Thr Trp Ser Gln
625                 630                 635                 640
Phe Ser Ala Arg Ile Phe Leu Arg Pro Ser Asn Val His Gln Val Thr
                645                 650                 655
Thr Leu Ser Val Gly Ile Val Val Leu Ile Ile Ser Phe Cys Leu Val
```

```
            660                 665                 670
Tyr Ile Ile Ser Ser Arg Ser Glu Val Leu Phe Glu Asp Leu Pro Ala
        675                 680                 685
Ser Asn Ala Ala Leu Phe Gly
    690                 695

      <210> 19
      <211> 17
      <212> PRT
      <213> human

      <400> 19
Ala Arg Leu Ala Arg Ala Leu Ser Pro Ala Phe Glu Leu Ser Gln Trp
 1               5                  10                  15
Ser
```